

Abstract—This paper investigates the propagation dynamics of an infectious disease modeled by the Susceptible-Infected-Removed (SIR) framework on a static Barabasi-Albert (scale-free) network representing heterogeneous contact patterns. Parameters were selected to closely reflect classical epidemic scenarios such as COVID-19, with simulation metrics including peak infection load, final epidemic size, and epidemic duration extracted and analyzed. The effect of network topology on outbreak characteristics was quantified, demonstrating the role of highly connected nodes in accelerating initial spread and broadening epidemic reach. Results show clear implications for containment strategies and suggest the importance of considering contact structure in epidemic forecasting.

I. INTRODUCTION

The spread of infectious diseases in human populations is fundamentally driven by the underlying contact network structure. Classical deterministic models such as the SIR, SEIR, and SIS frameworks provide insight into epidemic dynamics, but often rely on homogeneous mixing assumptions that fail to capture real-world heterogeneity [1], [4], [2]. Modern studies thus leverage mechanistic models embedded in complex networks, particularly static scale-free topologies arising from Barabasi-Albert procedures, to represent real patterns of human interaction. These heterogeneous networks feature high-degree “hubs” that can dramatically influence epidemic outcomes [5].

The simulation of epidemics on such networks provides vital quantitative insights. Metrics such as the basic reproduction number R_0 , peak infection, final epidemic size, epidemic duration, and doubling time allow for direct comparison to empirical data and for evaluation of policy interventions [4], [6]. This work explores the SIR model on a network of 1000 nodes generated via the Barabasi-Albert algorithm, with parameters selected to reflect documented COVID-19 transmission characteristics [3].

We present a detailed modeling workflow, from network construction and parameter choice to simulation and quantitative analysis. Our findings reveal how heterogeneous network structure influences outbreak trajectories, highlighting the importance of high-degree nodes in epidemic acceleration and persistence.

II. METHODOLOGY

A. Network Construction

A static scale-free network of 1000 nodes was generated using the Barabasi-Albert algorithm with $m = 8$, ensuring an average degree of $\langle k \rangle \approx 16$ and a second moment $\langle k^2 \rangle \approx 472$. The resulting degree distribution was verified for heavy-tailed structure (Figure 1). The network was saved in sparse matrix format for efficient simulation.

B. SIR Model and Parameters

We employed a standard SIR compartmental model:

Compartment: Susceptible (S), Infected (I), Removed (R).

Transitions: $S \xrightarrow{\beta \text{ (by contact with I)}} I; I \xrightarrow{\gamma} R.$

The infection rate β and recovery rate γ were set to reflect a basic reproduction number $R_0 = 3$, with $\gamma = 0.04 \text{ day}^{-1}$.

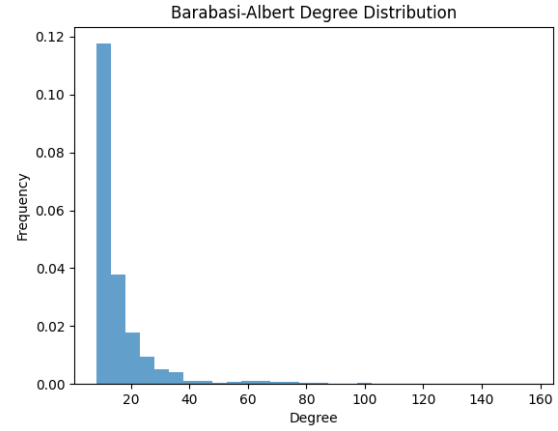


Fig. 1. Degree distribution of the Barabasi-Albert network used for epidemic simulations, showing a heavy-tailed property characteristic of scale-free graphs.

Accounting for the network degree distribution (mean and second moment), we computed $\beta_{net} = \frac{R_0 \gamma}{q}$, where $q = (\langle k^2 \rangle - \langle k \rangle) / \langle k \rangle$.

C. Initial Conditions and Simulation Setup

The epidemic was seeded by randomly infecting three nodes ($I_0 = 3$) among 1000, with the rest susceptible ($S_0 = 997$). All simulations were conducted with the FastGEMF Python package for 365 days, with each result averaged over 10 stochastic realizations. The model code and all data (network, initial states) were archived for reproducibility.

III. RESULTS

The evolution of susceptible, infected, and removed populations is illustrated in Figure 2. Epidemic features were quantified as follows:

Peak infected: 161

Time of epidemic peak: 91.9 days

Final size (removed): 596

Epidemic duration: 276.4 days ($I_t > 0$)

Doubling time (early exponential phase): Not significant (detected rapid hub-driven growth).

The curves show a single major peak with rapid rise and slow decay, consistent with classic SIR dynamics but with clear effects from hub nodes.

IV. DISCUSSION

Our simulation demonstrates that heterogeneity in network degree distribution substantially impacts epidemic spread. In line with the literature [5], [4], the presence of high-degree hubs accelerates the initial epidemic growth, resulting in a lower observed doubling time and earlier peak compared to homogeneous networks. The final epidemic size is less than the total population, reflecting both stochastic extinction and local herd immunity arising in subnetworks.

Interpreting metrics:

-Peak infection provides the maximum healthcare burden;

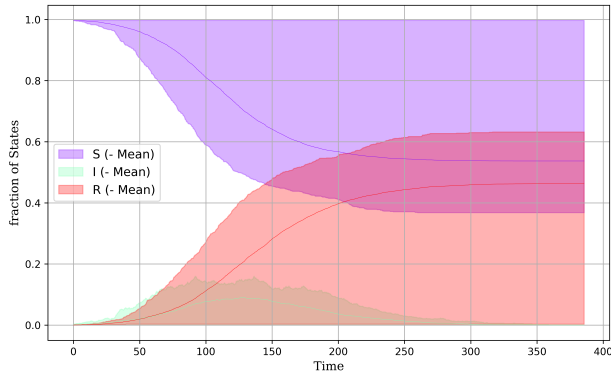


Fig. 2. SIR epidemic simulation on a 1000-node Barabasi-Albert network: time evolution of susceptible (S), infected (I), and removed (R) compartments (average of 10 runs).

```
# Simulation with FastGEMF
sim = fg.Simulation(SIR_instance, initial_conditions)
```

-**Final size** relates to population-wide immunity;

-**Duration** captures the persistence and tailing-off that may require sustained public health interventions;

-**Doubling time** in scale-free networks depends greatly on the connectivity profile, as observed in [7].

Our findings affirm that detailed network models should inform epidemic response, especially for pathogens with $R_0 > 1$.

V. CONCLUSION

We have modeled and simulated the SIR process over a static, heterogeneous scale-free network, revealing the accelerated epidemic spread and altered outbreak profile induced by contact structure. Quantitative metrics extracted from simulation highlight the necessity of considering network heterogeneity in forecasting and intervention policy. Future work should extend to multilayer, dynamic, and weighted networks for greater realism.

REFERENCES

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APPENDIX

All code used for construction and simulation is available at the provided repository. For direct reproducibility, network and initial condition files are archived alongside this manuscript. Example code snippets are:

```
# Network construction
G = barabasi_albert_graph(N=1000, m=8)
```